The following Listing of the Claims will replace all prior versions and all prior listings of the claims in the present application:

1.-8. (Canceled)

9. (Previously presented) The method of any one of claims 11 or 12,wherein said sample is a drop of blood.

10. (Previously presented) The method of any one of claims 11 or 12, wherein said blood sample is from a human.

11. (Currently amended) A method of identifying two or more genes differentially expressed in total blood cell RNA of blood samples which have not been fractionated into cell types ~~from~~ between subjects having a heart disease ~~as compared with~~and subjects not having said heart disease, said method comprising:

for each gene of a collection of two or more genes:

(a) using an oligonucleotide of predetermined sequence, detecting an amount of ~~an~~ RNA encoded by said gene in total blood cell RNA of blood samples which have not been fractionated into cell types ~~from subjects~~of subjects having said heart disease, said oligonucleotide being specific only for ~~said~~ RNA encoded by said gene, and/or for cDNA complementary to ~~said~~ RNA~~,~~ encoded by said gene in said samples, said gene being expressed in blood and in a heart tissue of a subject not having said heart disease;

(b) quantifying said amount of ~~said~~ RNA encoded by said gene in total blood cell RNA of said blood samples; and

(c) determining a difference between said quantified amount and a quantified amount of ~~said~~ RNA encoded by said gene in total blood cell RNA of control blood samples which have not been fractionated into cell types from control subjects, ~~said~~ RNA encoded by said gene having been detected in said samples from said control subjects,

thereby identifying each of said two or more genes as being differentially expressed in total blood cell RNA of blood samples which have not been fractionated into cell types ~~as~~ between subjects having ~~a~~ said heart disease and subjects not having said heart disease.

12. (Currently Amended) A method of identifying two or more genes differentially expressed in total blood cell RNA of blood samples which have not been fractionated into cell types ~~from~~between subjects having a heart disease ~~as compared with~~and subjects not having said heart disease, said method comprising:

for each gene of a collection of two or more genes:

(a) producing amplification products from ~~an~~ RNAencoded by said gene ~~from~~ in total blood cell RNA of blood samples which have not been fractionated into cell types ~~from~~ of subjects having said heart disease, using primers specific only for ~~said~~ RNA encoded by said gene, and/or for cDNA complementary to ~~said~~ RNA, encoded by said gene in said samples, said gene being expressed in blood and in heart tissue of a subject not having said heart disease;

(b) quantifying an amount of said amplification products ~~of said RNA encoded by said gene in total blood cell RNA of said blood samples~~; and

(c) determining a difference between said ~~quantity~~ amount of said amplification products and a quantity of amplification products produced from RNA encoded by said gene ~~from~~ in total blood cell RNA of control blood samples which have not been fractionated into cell types from control subjects, ~~said amplification products of said control samples having been detected in said samples~~ using primers specific only for ~~said~~ RNA encoded by said gene, and/or for cDNA complementary to ~~said~~ RNA~~,~~ encoded by said gene in said control samples;

thereby identifying said two or more genes as being differentially expressed in total blood cell RNA of blood samples which have not been fractionated into cell types ~~from~~ between subjects having ~~a~~ said heart disease ~~as compared with~~and subjects not having said heart disease.

13. (New) A method for detecting expression of a gene in a human test subject, wherein said gene is selected from the group consisting of: beta myosin heavy chain (β MyHC), atrial natriuretic factor (ANF) and zinc finger protein (ZFP), said method comprising

detecting RNA encoded by said gene in a blood sample from said test subject, using an oligonucleotide of predetermined sequence which is specific for RNA encoded by said gene, and/or for cDNA complementary to RNA encoded by said gene in said sample.

14. (New) The method of claim 13, wherein said detecting expression of said gene in said human test subject comprises producing an amplification product from RNA encoded by said gene in said blood sample from said test subject, using primers specific only for RNA encoded by said gene, and/or for cDNA complementary to RNA encoded by said gene in said sample.

15. (New) The method of claim 13 or claim 14, wherein said method further comprises quantifying a level of RNA encoded by said gene in said sample.

16. (New) The method of claim 13 or claim 14 wherein said gene is an ANF gene.

17. (New) The method of claim 15, wherein said gene is an ANF gene.

18. (New) The method of claim 15, further comprising comparing said level of RNA encoded by said gene in said sample to a quantified level of control RNA encoded by said gene in blood samples of control subjects.

19 (New) The method of claim 18, wherein said gene is an ANF gene and said control subjects are selected from the group consisting of: normal healthy subjects and patients with heart failure.

20. (New) The method of claim 19, wherein said control subjects are normal healthy subjects.

21. (New) The method of claim 20, further comprising identifying said test subject as being a candidate for having or being predisposed to heart failure if the comparison shows that said level of RNA encoded by said ANF gene in said blood sample of said

human test subject is significantly higher than said quantified level of RNA encoded by said gene in said blood samples of said normal healthy subjects.

22. (New) A method of screening a human test subject for being a candidate for having or being predisposed to heart failure, said method comprising

(a) detecting RNA encoded by an ANF gene in a blood sample of said test subject, using an oligonucleotide of predetermined sequence which is specific for RNA encoded by said gene, and/or for cDNA complementary to RNA encoded by said gene; and

(b) quantifying a level of said RNA encoded by said gene in said sample; and

(c) comparing said level to a quantified level of control RNA encoded by said gene in blood samples of normal healthy control subjects;

wherein said test subject is a candidate for having or being predisposed to heart failure if the comparison of step (c) shows that said level of RNA encoded by said gene in said blood sample of said human test subject is significantly higher than said quantified level of control RNA encoded by said gene in said samples of said normal healthy subjects.

23. (New) The method of claim 13 or claim 14, wherein said gene is a ZFP gene.

24. (New) The method of claim 15, wherein said gene is a ZFP gene.

25. (New) The method of claim 18, wherein said gene is a ZFP gene, and wherein said control subjects are selected from the group consisting of: normal healthy subjects, patients with heart failure and patients with cardiac hypertrophy.

26. (New) The method of claim 25, wherein said control subjects are normal healthy subjects.

27. (New) The method of claim 26, further comprising identifying said test subject as being a candidate for having or being predisposed to heart failure or cardiac hypertrophy if the comparison of step (c) shows that said level of RNA encoded by said gene in said

blood sample of said human test subject is significantly higher than said quantified level of control RNA encoded by said gene in said samples of said normal healthy subjects.

28. (New) The method of claim 27, wherein said test subject is an asymptomatic diabetic.

29. (New) A method of screening a test subject for being a candidate for having or being predisposed to heart failure, said method comprising

(a) detecting RNA encoded by a ZFP gene in a blood sample of said test subject, using an oligonucleotide of predetermined sequence which is specific for RNA encoded by said gene, and/or for cDNA complementary to RNA encoded by said gene in said sample; and

(b) quantifying a level of RNA encoded by said ZFP gene in said sample; and

(c) comparing said level to a quantified level of control RNA encoded by said gene in blood samples of normal healthy control subjects;

wherein said test subject is a candidate for having or being predisposed to heart failure if the comparison of step (c) shows that said level of RNA encoded by said gene in said blood sample of said human test subject is significantly higher than said quantified level of control RNA encoded by said gene in said blood samples of said normal healthy control subjects.

30. (New) The method of claim 17, wherein said test subject is an asymptomatic diabetic.

31. (New) The method of claim 13 or claim 14, wherein said gene is a beta-myosin heavy chain gene.

32. (New) The method of claim 13 or claim 14, wherein said gene is a beta-myosin heavy chain gene, said method further comprising detecting one or more mutations associated with familial hypertrophic cardiomyopathy in said gene in said test subject.

33. (New) The method of claim 32, wherein said mutation is a missense mutation of arginine residue 403 to a glutamine.

34. (New) The method of claim 14, wherein said gene is a beta-myosin heavy chain gene, and said primers include a first primer with a nucleic acid sequence of SEQ ID NO:3 and a second primer with a nucleic acid sequence of SEQ ID NO:4.

35. (New) The method of claim 14, wherein said gene is a ZFP gene, and said primers include a first primer with a nucleic acid sequence of SEQ ID NO:9 and a second primer with a nucleic acid sequence of SEQ ID NO:10.

36. (New) The method of claim 14, wherein said gene is ANF, and said primers include a first primer with a nucleic acid sequence of SEQ ID NO:5 and a second primer with a nucleic acid sequence of SEQ ID NO:6.

37. (New) The method of claim 13 or claim 14, wherein said blood sample is selected from the group consisting of: a whole blood sample, a blood sample which has not been fractionated into cell types, and a blood sample which comprises leukocytes which have not been fractionated into cell types.

38. (New) The method of claim 15, wherein said blood sample is selected from the group consisting of: a whole blood sample, a blood sample in which has not been fractionated into cell types, and a blood sample which comprises leukocytes which have not been fractionated into cell types.

39. (New) The method of claim 13 or claim 14, wherein said gene is a ZFP gene, and wherein said blood sample is selected from the group consisting of: granulocytes, monocytes, CD19+ cells and CD3+ cells.

40. (New) The method of claim 15, wherein said gene is a ZFP gene, and wherein said blood sample is selected from the group consisting of: granulocytes, monocytes, CD19+ cells and CD3+ cells.

41. (New) The method of claim 18, wherein:

(i) said blood sample of said test subject and said blood samples of said control subjects are whole blood samples; or

(ii) said blood sample of said test subject and said blood samples of said control subjects are blood samples which have not been fractionated into cell types; or

(iii) said blood sample of said test subject and said blood samples of said control subjects are blood samples which comprise leukocytes which have not been fractionated into cell types.

42. (New) The method of claim 22 or claim 29, wherein:

(i) said blood sample of said test subject and said blood samples of said control subjects are whole blood samples; or

(ii) said blood sample of said test subject and said blood samples of said control subjects are blood samples which have not been fractionated into cell types; or

(iii) said blood sample of said test subject and said blood samples of said control subjects are blood samples which comprise leukocytes which have not been fractionated into cell types.

43. (New) The method of claim 15, wherein said quantifying of said level of RNA encoded by said gene is effected by:

(i) quantifying said level of RNA encoded by said gene relative to a housekeeping gene; or

(ii) quantification of cDNA corresponding to RNA encoded by said gene; or

(iii) using quantitative real-time RT-PCR; or

(iv) using an array.